

## SEQUENCE LISTING

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<120> Nucleic Acid Vaccines Against Rickettsial Diseases and  
 Methods of use

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<150> 09/337,827  
 <151> 1999-06-22

<150> 08/953,326  
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<170> PatentIn Ver. 2.0

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aac cca gca ggc agt gtt tac att agc gca aaa tac atg cca act gca	144
Asn Pro Ala Gly Ser Val Tyr Ile Ser Ala Lys Tyr Met Pro Thr Ala	
35 40 45	
tca cat ttt ggt aaa atg tca atc aaa gaa gat tca aaa aat act caa	192
Ser His Phe Gly Lys Met Ser Ile Lys Glu Asp Ser Lys Asn Thr Gln	
50 55 60	
acg gta ttt ggt cta aaa aaa gat tgg gat ggc gtt aaa aca cca tca	240
Thr Val Phe Gly Leu Lys Lys Asp Trp Asp Gly Val Lys Thr Pro Ser	
65 70 75 80	
gat tct agc aat act aat tct aca att ttt act gaa aaa gac tat tct	288
Asp Ser Ser Asn Thr Asn Ser Thr Ile Phe Thr Glu Lys Asp Tyr Ser	
85 90 95	
ttc aga tat gaa aac aat ccg ttt tta ggt ttc gct gga gca att ggg	336
Phe Arg Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly	
100 105 110	
tac tca atg aat gga cca aga ata gag ttc gaa gta tcc tat gaa act	384
Tyr Ser Met Asn Gly Pro Arg Ile Glu Phe Glu Val Ser Tyr Glu Thr	
115 120 125	
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130 135 140	
tac tgt gct tta gat aca gca gca caa aat agc act aat ggc gca gga	480
Tyr Cys Ala Leu Asp Thr Ala Ala Gln Asn Ser Thr Asn Gly Ala Gly	
145 150 155 160	
tta act aca tct gtt atg gta aaa aac gaa aat tta aca aat ata tca	528
Leu Thr Thr Ser Val Met Val Lys Asn Glu Asn Leu Thr Asn Ile Ser	
165 170 175	
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Leu Met Leu Asn Ala Cys Tyr Asp Ile Met Leu Asp Gly Ile Pro Val	
180 185 190	
tct cca tat gta tgt gca ggt att ggc act gac tta gtg tca gta att	624
Ser Pro Tyr Val Cys Ala Gly Ile Gly Thr Asp Leu Val Ser Val Ile	
195 200 205	
aat gct aca aat cct aaa tta tct tat caa gga aag cta ggc ata agt	672
Asn Ala Thr Asn Pro Lys Leu Ser Tyr Gln Gly Lys Leu Gly Ile Ser	
210 215 220	
tac tca atc aat tct gaa gct tct atc ttt atc ggt gga cat ttc cat	720
Tyr Ser Ile Asn Ser Glu Ala Ser Ile Phe Ile Gly Gly His Phe His	
225 230 235 240	

aga gtt ata ggt aat gaa ttt aaa gat att gct acc tta aaa ata ttt 768  
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act tca aaa aca gga ata tct aat cct ggc ttt gca tca gca aca ctt 816  
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Tyr Ser Ile Asn Ser Glu Ala Ser Ile Phe Ile Gly Gly His Phe His  
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Arg Val Ile Gly Asn Glu Phe Lys Asp Ile Ala Thr Leu Lys Ile Phe  
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<222> (1)..(840)

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 Ile Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Asp Ala Lys Ala Ser  
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cat ttt gga gta ttc tct gct aag gaa gaa aga aat aca aca gtt gga 192  
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 65 70 75 80

tcc cca aac gat gta ttc act gtc tca aat tat tca ttt aaa tat gaa 288  
 Ser Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu  
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aac aac ccg ttt tta ggt ttt gca gga gct att ggt tac tca atg gat 336  
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tgc tat gac gta gta ggc gaa ggc ata cct ttt tct cct tat ata tgc 576
Cys Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys
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Ala Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro
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aaa att tct tac caa gga aag tta ggt tta agc tac tct ata agc cca 672
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gaa ttt aga gat att cct act ata ata cct act gga tca aca ctt gca 768
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gga aaa gga aac tac cct gca ata gta ata ctg gat gta tgc cac ttt 816
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&lt;211&gt; 849

&lt;212&gt; DNA

&lt;213&gt; Anaplasma marginale

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&lt;222&gt; (1)..(846)

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85 90 95	
ggc tac act ttt gcc ttc tct aaa aac tta atc acg tct ttc gac ggc	336
Gly Tyr Thr Phe Ala Phe Ser Lys Asn Leu Ile Thr Ser Phe Asp Gly	
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gct gtg gga tat tct ctg gga gga gcc aga gtg gaa ttg gaa gcg agc	384
Ala Val Gly Tyr Ser Leu Gly Gly Ala Arg Val Glu Leu Glu Ala Ser	
115 120 125	
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Tyr Arg Arg Phe Ala Thr Leu Ala Asp Gly Gln Tyr Ala Lys Ser Gly	
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gcg gaa tct ctg gca gct att acc cgc gac gct aac att act gag acc	480
Ala Glu Ser Leu Ala Ala Ile Thr Arg Asp Ala Asn Ile Thr Glu Thr	
145 150 155 160	
aat tac ttc gta gtc aaa att gat gaa atc aca aac acc tca gtc atg	528
Asn Tyr Phe Val Val Lys Ile Asp Glu Ile Thr Asn Thr Ser Val Met	
165 170 175	
tta aat ggc tgc tat gac gtg ctg cac aca gat tta cct gtg tcc ccg	576
Leu Asn Gly Cys Tyr Asp Val Leu His Thr Asp Leu Pro Val Ser Pro	
180 185 190	
tat gta tgt gcc ggg ata ggc gca agc ttt gtt gac atc tct aag caa	624
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225                230                235                240

ttt gat gag tct tac aag gac att ccc gca cac aac agt gta aag ttc 768
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                245                250                255

tct gga gaa gca aaa gcc tca gtc aaa gcg cat att gct gac tac ggc 816
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Met Arg Glu Ser Ser Lys Glu Thr Ser Tyr Val Arg Gly Tyr Asp Lys
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Ser Ile Ala Thr Ile Asp Val Ser Val Pro Ala Asn Phe Ser Lys Ser
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Ala Val Gly Tyr Ser Leu Gly Gly Ala Arg Val Glu Leu Glu Ala Ser
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Val Thr Thr Lys Leu Ala Tyr Arg Gly Lys Val Gly Ile Ser Tyr Gln			
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Phe Thr Pro Glu Ile Ser Leu Val Ala Gly Gly Phe Tyr His Gly Leu			
	225	230	235
Phe Asp Glu Ser Tyr Lys Asp Ile Pro Ala His Asn Ser Val Lys Phe			
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Ser Gly Glu Ala Lys Ala Ser Val Lys Ala His Ile Ala Asp Tyr Gly			
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attgtgctct atcccataac tcagcagcag acatgagtag tgcaagtaat aattttgtct 480  
 ttctaaaaaa tgaaggatta cttgacatat catttatgct gaacgcatgc tatgacgtag 540  
 taggcgaagg catacctttt tctccttata tatgcgagcagg tatcggtact gatttagtat 600  
 ccatgtttga agctacaaat cctaaaattt cttaccaagg aaagttaggt ttaagctact 660  
 ctataagccc agaagcttct gtgtttattg gtgggcactt tcataaggta atagggaacg 720  
 aatttagaga tattcctact ataataccta ctggatcaac acttgcagga aaaggaaact 780  
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<210> 12

<211> 864

<212> DNA

<213> Ehrlichia canis

<400> 12

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 attttatacc tttttatagt ccagcacgtg ccagtacaat tcacaacttc tacattagt 120  
 gaaaatatat gccaacagcg tcacattttg gaattttttc agctaaagaa gaacaaagtt 180  
 ttactaagggt attagttggg ttagatcaac gattatcaca taatattata aacaataatg 240  
 atacagcaaa gagtcttaag gttcaaaatt attcatttaa atacaaaaat aaccatttc 300  
 taggatttgc aggagctatt gggtattcaa taggcaattc aagaatagaa ctagaagtat 360  
 cacatgaaat atttgatact aaaaaccag gaaacaatta tttaaatgac tctcacaat 420  
 attgcgcttt atctcatgga agtcacatat gcagtgatgg aaatagcgga gattggtaca 480  
 ctgcaaaaac tgataagttt gtacttctga aaaatgaagg tttacttgac gtctcattta 540  
 tgttaaacgc atgttatgac ataacaactg aaaaaatgcc tttttcacct tatatatgtg 600  
 caggatttgg tactgatctc atatctatgt ttgagacaac acaaaacaaa atatcttata 660  
 aaggaaagtt aggtttaaac tatactataa actcaagagt ttctgttttt gcagggtgggc 720  
 actttcataa ggtaatagggt aatgaattta aaggatttcc tactctatta cctgatggat 780  
 caaacattaa agtacaacag tctgcaacag taacattaga tgtgtgccat ttcggggttag 840  
 agattggaag tagatttttc tttt 864

<210> 13

<211> 399

<212> DNA

<213> Ehrlichia canis

<400> 13

atatgaattg taaaaaagtt ttcacaataa gtgcattgat atcatccata tacttcttac 60  
 ctaatgtctc atactctaac ccagtatatg gtaacagtat gtatggtaat ttttacatat 120  
 caggaaagta catgccaaagt gttcctcatt ttggaatttt ttcagctgaa gaagagaaaa 180  
 aaaagacaac tgtagtatat ggcttaaaag aaaactgggc aggagatgca atatctagtc 240  
 aaagtccaga tgataatttt accattcgaa attactcatt caagtatgca agcaacaagt 300  
 ttttaggggtt tgcagtagct attgggttact cgataggcag tccaagaata gaagttgaga 360  
 tgtcttatga agcatttgat gtaaaaaatc aaggttaaca 399

<210> 14

<211> 43

<212> PRT

<213> Ehrlichia chaffeensis

<400> 14

Asn	Glu	Phe	Arg	Asp	Ile	Ser	Thr	Leu	Lys	Ala	Phe	Ala	Thr	Pro	Ser
1				5					10					15	
Ser	Ala	Ala	Thr	Pro	Asp	Leu	Ala	Thr	Val	Thr	Leu	Ser	Val	Cys	His
			20					25					30		
Phe	Gly	Val	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe					
		35					40								

<210> 15

<211> 286

<212> PRT

<213> Ehrlichia chaffeensis

<400> 15

Met	Asn	Cys	Glu	Lys	Phe	Phe	Ile	Thr	Thr	Ala	Leu	Thr	Leu	Leu	Met
1				5					10					15	
Ser	Phe	Leu	Pro	Gly	Ile	Ser	Leu	Ser	Asp	Pro	Val	Gln	Asp	Asp	Asn
			20					25					30		
Ile	Ser	Gly	Asn	Phe	Tyr	Ile	Ser	Gly	Lys	Tyr	Met	Pro	Ser	Ala	Ser
		35					40					45			
His	Phe	Gly	Val	Phe	Ser	Ala	Lys	Glu	Glu	Arg	Asn	Thr	Thr	Val	Gly
	50					55					60				
Val	Phe	Gly	Ile	Glu	Gln	Asp	Trp	Asp	Arg	Cys	Val	Ile	Ser	Arg	Thr
65					70				75					80	
Thr	Leu	Ser	Asp	Ile	Phe	Thr	Val	Pro	Asn	Tyr	Ser	Phe	Lys	Tyr	Glu

85					90					95					
Asn	Asn	Leu	Phe	Ser	Gly	Phe	Ala	Gly	Ala	Ile	Gly	Tyr	Ser	Met	Asp
		100						105					110		
Gly	Pro	Arg	Ile	Glu	Leu	Glu	Val	Ser	Tyr	Glu	Ala	Phe	Asp	Val	Lys
		115					120					125			
Asn	Gln	Gly	Asn	Asn	Tyr	Lys	Asn	Glu	Ala	His	Arg	Tyr	Tyr	Ala	Leu
	130					135					140				
Ser	His	Leu	Leu	Gly	Thr	Glu	Thr	Gln	Ile	Asp	Gly	Ala	Gly	Ser	Ala
145					150					155					160
Ser	Val	Phe	Leu	Ile	Asn	Glu	Gly	Leu	Leu	Asp	Lys	Ser	Phe	Met	Leu
			165						170					175	
Asn	Ala	Cys	Tyr	Asp	Val	Ile	Ser	Glu	Gly	Ile	Pro	Phe	Ser	Pro	Tyr
			180						185					190	
Ile	Cys	Ala	Gly	Ile	Gly	Ile	Asp	Leu	Val	Ser	Met	Phe	Glu	Ala	Ile
		195					200					205			
Asn	Pro	Lys	Ile	Ser	Tyr	Gln	Gly	Lys	Leu	Gly	Leu	Ser	Tyr	Pro	Ile
	210					215					220				
Ser	Pro	Glu	Ala	Ser	Val	Phe	Ile	Gly	Gly	His	Phe	His	Lys	Val	Ile
225					230					235					240
Gly	Asn	Glu	Phe	Arg	Asp	Ile	Pro	Thr	Met	Ile	Pro	Ser	Glu	Ser	Ala
			245						250					255	
Leu	Ala	Gly	Lys	Gly	Asn	Tyr	Pro	Ala	Ile	Val	Thr	Leu	Asp	Val	Phe
		260						265					270		
Tyr	Phe	Gly	Ile	Glu	Leu	Gly	Gly	Arg	Phe	Asn	Phe	Gln	Leu		
		275					280					285			

&lt;210&gt; 16

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia chaffeensis

&lt;400&gt; 16

Met	Asn	Cys	Lys	Lys	Phe	Phe	Ile	Thr	Thr	Ala	Leu	Val	Ser	Leu	Met
1				5					10					15	

Ser	Phe	Leu	Pro	Gly	Ile	Ser	Phe	Ser	Asp	Pro	Val	Gln	Gly	Asp	Asn
		20					25						30		

Ile	Ser	Gly	Asn	Phe	Tyr	Val	Ser	Gly	Lys	Tyr	Met	Pro	Ser	Ala	Ser
		35					40					45			

His	Phe	Gly	Met	Phe	Ser	Ala	Lys	Glu	Glu	Lys	Asn	Pro	Thr	Val	Ala
		50				55					60				

Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His  
 65 70 75 80  
 Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn  
 85 90 95  
 Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly  
 100 105 110  
 Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn  
 115 120 125  
 Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly  
 130 135 140  
 Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu  
 145 150 155 160  
 Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr  
 165 170 175  
 Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly  
 180 185 190  
 Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile  
 195 200 205  
 Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala  
 210 215 220  
 Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe  
 225 230 235 240  
 Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro  
 245 250 255  
 Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu  
 260 265 270  
 Gly Gly Arg Phe Asn Phe  
 275

&lt;210&gt; 17

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia chaffeensis

&lt;400&gt; 17

Met Asn Cys Lys Lys Phe Phe Ile Thr Thr Thr Leu Val Ser Leu Met  
 1 5 10 15

Ser Phe Leu Pro Gly Ile Ser Phe Ser Asp Ala Val Gln Asn Asp Asn  
 20 25 30

Val Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro Ser Val Ser  
           35                                  40                                  45

His Phe Gly Val Phe Ser Ala Lys Gln Glu Arg Asn Thr Thr Ile Gly  
       50                                  55                                  60

Val Phe Gly Leu Lys Gln Asp Trp Asp Gly Ser Thr Ile Ser Lys Asn  
       65                                  70                                  75                                  80

Ser Pro Glu Asn Thr Phe Asn Val Pro Asn Tyr Ser Phe Lys Tyr Glu  
                                   85                                  90                                  95

Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala Val Gly Tyr Leu Met Asn  
                                   100                                  105                                  110

Gly Pro Arg Ile Glu Leu Glu Met Ser Tyr Glu Thr Phe Asp Val Lys  
                                   115                                  120                                  125

Asn Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Lys Tyr Tyr Ala Leu  
       130                                  135                                  140

Thr His Asn Ser Gly Gly Lys Leu Ser Asn Ala Gly Asp Lys Phe Val  
       145                                  150                                  155                                  160

Phe Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Leu Met Leu Asn Ala  
                                   165                                  170                                  175

Cys Tyr Asp Val Ile Ser Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys  
                                   180                                  185                                  190

Ala Gly Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Ile Asn Pro  
                                   195                                  200                                  205

Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro  
       210                                  215                                  220

Glu Ala Ser Val Phe Val Gly Gly His Phe His Lys Val Ile Gly Asn  
       225                                  230                                  235                                  240

Glu Phe Arg Asp Ile Pro Ala Met Ile Pro Ser Thr Ser Thr Leu Thr  
                                   245                                  250                                  255

Gly Asn His Phe Thr Ile Val Thr Leu Ser Val Cys His Phe Gly Val  
                                   260                                  265                                  270

Glu Leu Gly Gly Arg Phe Asn Phe  
       275                                  280

<210> 18

<211> 276

<212> PRT

<213> Ehrlichia chaffeensis

<400> 18

Met Asn Tyr Lys Lys Val Phe Ile Thr Ser Ala Leu Ile Ser Leu Ile



1	5	10	15
Ser Ser Leu Pro Gly Val Ser Phe Ser Asp Pro Ala Gly Ser Gly Ile	20	25	30
Asn Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Ala Ser His	35	40	45
Phe Gly Val Phe Ser Ala Lys Glu Glu Arg Asn Thr Thr Val Gly Val	50	55	60
Phe Gly Leu Lys Gln Asn Trp Asp Gly Ser Ala Ile Ser Asn Ser Ser	65	70	75
Pro Asn Asp Val Phe Thr Val Ser Asn Tyr Ser Phe Lys Tyr Glu Asn	85	90	95
Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Asp Gly	100	105	110
Pro Arg Ile Glu Leu Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn	115	120	125
Gln Gly Asn Asn Tyr Lys Asn Glu Ala His Arg Tyr Cys Ala Leu Ser	130	135	140
His Asn Ser Ala Ala Asp Met Ser Ser Ala Ser Asn Asn Phe Val Phe	145	150	155
Leu Lys Asn Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys	165	170	175
Tyr Asp Val Val Gly Glu Gly Ile Pro Phe Ser Pro Tyr Ile Cys Ala	180	185	190
Gly Ile Gly Thr Asp Leu Val Ser Met Phe Glu Ala Thr Asn Pro Lys	195	200	205
Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Ser Pro Glu	210	215	220
Ala Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu	225	230	235
Phe Arg Asp Ile Pro Thr Ile Ile Pro Thr Gly Ser Thr Leu Ala Gly	245	250	255
Lys Gly Asn Tyr Pro Ala Ile Val Ile Leu Asp Val Cys His Phe Gly	260	265	270
Ile Glu Met Gly	275		

&lt;210&gt; 19

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia canis

&lt;400&gt; 19

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Met Lys Tyr Lys Lys Thr Phe Thr Val Thr Ala Leu Val Leu Leu Thr
 1             5             10             15

Ser Phe Thr His Phe Ile Pro Phe Tyr Ser Pro Ala Arg Ala Ser Thr
          20             25             30

Ile His Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Thr Ala Ser His
      35             40             45

Phe Gly Ile Phe Ser Ala Lys Glu Glu Gln Ser Phe Thr Lys Val Leu
 50             55             60

Val Gly Leu Asp Gln Arg Leu Ser His Asn Ile Ile Asn Asn Asn Asp
 65             70             75             80

Thr Ala Lys Ser Leu Lys Val Gln Asn Tyr Ser Phe Lys Tyr Lys Asn
          85             90             95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Ile Gly Asn
      100             105             110

Ser Arg Ile Glu Leu Glu Val Ser His Glu Ile Phe Asp Thr Lys Asn
      115             120             125

Pro Gly Asn Asn Tyr Leu Asn Asp Ser His Lys Tyr Cys Ala Leu Ser
      130             135             140

His Gly Ser His Ile Cys Ser Asp Gly Asn Ser Gly Asp Trp Tyr Thr
      145             150             155             160

Ala Lys Thr Asp Lys Phe Val Leu Leu Lys Asn Glu Gly Leu Leu Asp
          165             170             175

Val Ser Phe Met Leu Asn Ala Cys Tyr Asp Ile Thr Thr Glu Lys Met
          180             185             190

Pro Phe Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp Leu Ile Ser
          195             200             205

Met Phe Glu Thr Thr Gln Asn Lys Ile Ser Tyr Gln Gly Lys Leu Gly
      210             215             220

Leu Asn Tyr Thr Ile Asn Ser Arg Val Ser Val Phe Ala Gly Gly His
      225             230             235             240

Phe His Lys Val Ile Gly Asn Glu Phe Lys Gly Ile Pro Thr Leu Leu
          245             250             255

Pro Asp Gly Ser Asn Ile Lys Val Gln Gln Ser Ala Thr Val Thr Leu
          260             265             270

Asp Val Cys His Phe Gly Leu Glu Ile Gly Ser Arg Phe Phe Phe

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275

280

285

<210> 20  
 <211> 133  
 <212> PRT  
 <213> Ehrlichia canis

<400> 20  
 Met Asn Cys Lys Lys Val Phe Thr Ile Ser Ala Leu Ile Ser Ser Ile  
     1                    5                    10                    15  
 Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly Asn Ser  
                     20                    25                    30  
 Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro Ser Val Pro  
                     35                    40                    45  
 His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys Lys Thr Thr Val  
     50                    55                    60  
 Val Tyr Gly Leu Lys Glu Asn Trp Ala Gly Asp Ala Ile Ser Ser Gln  
     65                    70                    75                    80  
 Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn Tyr Ser Phe Lys Tyr Ala  
                     85                    90                    95  
 Ser Asn Lys Phe Leu Gly Phe Ala Val Ala Ile Gly Tyr Ser Ile Gly  
                     100                    105                    110  
 Ser Pro Arg Ile Glu Val Glu Met Ser Tyr Glu Ala Phe Asp Val Lys  
                     115                    120                    125  
 Asn Gln Gly Asn Asn  
     130

<210> 21  
 <211> 686  
 <212> DNA  
 <213> Ehrlichia canis

<400> 21  
 atgaaagcta tcaaattcat acttaatgtc tgcttactat ttgcagcaat attttttaggg 60  
 tattcctata ttacaaaaca aggcataattt caaacaaaac atcatgatac acctaatact 120  
 actataccaa atgaagacgg tattcaatct agcttttagct taatcaatca agacggtaaa 180  
 acagtaacca gccaaagattt cctagggaaa cacatgttag ttttgtttgg attctctgca 240  
 tgtaaaagca tttgccctgc agaattggga ttagtatctg aagcacttgc acaacttgggt 300  
 aataatgcag acaaattaca agtaattttt attacaattg atccaaaaaa tgatactgta 360  
 gaaaaattaa aagaatttca tgaacatttt gattcaagaa ttcaaattgtt aacaggaaat 420

actgaagaca ttaatcaaat aattaaaaat tataaaatat atgttggaca agcagataaa 480  
gatcatcaaa ttaaccattc tgcaataatg taccttattg aaaaaaagg atcatatctt 540  
tcacacttca ttccagattt aaaatcacaa gaaaatcaag tagataagtt actatcttta 600  
gttaagcagt atctgtaaat aaattcatgg aatacgttgg atgagtaggt ttttttagt 660  
atttttagtg ctaataacat tggcat 686

<210> 22  
<211> 618  
<212> DNA  
<213> *Ehrlichia chaffeensis*

<400> 22  
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tattcctacg taacaaaaca aggcattttt caagtaagag atcataaacac tccaatata 120  
aatatatcaa ataaagccag cattactact agtttttcgt tagtaaataca agatggaaat 180  
acagtaaata gtcaagattt tttgggaaaa tacatgctag ttttatttgg attttcttca 240  
tgtaaaagca tctgccctgc tgaattagga atagcatctg aagttctctc acagcttggt 300  
aatgacacag acaagttaca agtaattttc attacaattg atccaacaaa tgatactgta 360  
caaaaattaa aaacatttca tgaacatttt gatcctagaa ttcaaagct aacaggcagt 420  
gcagaagata ttgaaaaaat aataaaaaat tacaaaatat atgttggaca agcagataaa 480  
gataatcaaa ttgatcactc tgccataatg tacattatcg ataaaaagg agaatacatt 540  
tcacactttt ctccagattt aaaatcaaca gaaaatcaag tagataagtt actatctata 600  
ataaaacaat atctctaa 618

<210> 23  
<211> 205  
<212> PRT  
<213> *Ehrlichia canis*

<400> 23  
Met Lys Ala Ile Lys Phe Ile Leu Asn Val Cys Leu Leu Phe Ala Ala  
1 5 10 15  
Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Thr  
20 25 30  
Lys His His Asp Thr Pro Asn Thr Thr Ile Pro Asn Glu Asp Gly Ile  
35 40 45

Gln Ser Ser Phe Ser Leu Ile Asn Gln Asp Gly Lys Thr Val Thr Ser  
 50 55 60  
 Gln Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ala  
 65 70 75 80  
 Cys Lys Ser Ile Cys Pro Ala Glu Leu Gly Leu Val Ser Glu Ala Leu  
 85 90 95  
 Ala Gln Leu Gly Asn Asn Ala Asp Lys Leu Gln Val Ile Phe Ile Thr  
 100 105 110  
 Ile Asp Pro Lys Asn Asp Thr Val Glu Lys Leu Lys Glu Phe His Glu  
 115 120 125  
 His Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Thr Glu Asp Ile  
 130 135 140  
 Asn Gln Ile Ile Lys Asn Tyr Lys Ile Tyr Val Gly Gln Ala Asp Lys  
 145 150 155 160  
 Asp His Gln Ile Asn His Ser Ala Ile Met Tyr Leu Ile Asp Lys Lys  
 165 170 175  
 Gly Ser Tyr Leu Ser His Phe Ile Pro Asp Leu Lys Ser Gln Glu Asn  
 180 185 190  
 Gln Val Asp Lys Leu Leu Ser Leu Val Lys Gln Tyr Leu  
 195 200 205

<210> 24

<211> 205

<212> PRT

<213> Ehrlichia chaffeensis

<400> 24

Met Lys Val Ile Lys Phe Ile Leu Asn Ile Cys Leu Leu Phe Ala Ala  
 1 5 10 15  
 Ile Phe Leu Gly Tyr Ser Tyr Val Thr Lys Gln Gly Ile Phe Gln Val  
 20 25 30  
 Arg Asp His Asn Thr Pro Asn Thr Asn Ile Ser Asn Lys Ala Ser Ile  
 35 40 45  
 Thr Thr Ser Phe Ser Leu Val Asn Gln Asp Gly Asn Thr Val Asn Ser  
 50 55 60  
 Gln Asp Phe Leu Gly Lys Tyr Met Leu Val Leu Phe Gly Phe Ser Ser  
 65 70 75 80  
 Cys Lys Ser Ile Cys Pro Ala Glu Leu Gly Ile Ala Ser Glu Val Leu  
 85 90 95  
 Ser Gln Leu Gly Asn Asp Thr Asp Lys Leu Gln Val Ile Phe Ile Thr

100	105	110
Ile Asp Pro Thr Asn Asp Thr Val Gln Lys Leu Lys Thr Phe His Glu		
115	120	125
His Phe Asp Pro Arg Ile Gln Met Leu Thr Gly Ser Ala Glu Asp Ile		
130	135	140
Glu Lys Ile Ile Lys Asn Tyr Lys Ile Tyr Val Gly Gln Ala Asp Lys		
145	150	155
Asp Asn Gln Ile Asp His Ser Ala Ile Met Tyr Ile Ile Asp Lys Lys		
165	170	175
Gly Glu Tyr Ile Ser His Phe Ser Pro Asp Leu Lys Ser Thr Glu Asn		
180	185	190
Gln Val Asp Lys Leu Leu Ser Ile Ile Lys Gln Tyr Leu		
195	200	205

&lt;210&gt; 25

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Cowdria ruminantium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(615)

&lt;400&gt; 25

atg aag gct atc aag ttt ata ctt aat cta tgt tta cta ttt gca gca	48
Met Lys Ala Ile Lys Phe Ile Leu Asn Leu Cys Leu Leu Phe Ala Ala	
1 5 10 15	
att ttt ttg gga tat tct tac ata aca aaa caa ggt ata ttc caa cca	96
Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Pro	
20 25 30	
aaa tta cac gac tct cct gat gtt aat ata tcg aac aaa gcg gat ata	144
Lys Leu His Asp Ser Pro Asp Val Asn Ile Ser Asn Lys Ala Asp Ile	
35 40 45	
aat act agc ttt agc tta att aat cag gat ggt att acg ata tct agt	192
Asn Thr Ser Phe Ser Leu Ile Asn Gln Asp Gly Ile Thr Ile Ser Ser	
50 55 60	
aaa gac ttc ctt gga aaa cat atg tta gtc ctt ttt ggg ttt tct tct	240
Lys Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ser	
65 70 75 80	
tgt aaa act att tgc ccc atg gaa cta ggg tta gca tcc aca att cta	288
Cys Lys Thr Ile Cys Pro Met Glu Leu Gly Leu Ala Ser Thr Ile Leu	
85 90 95	
gat caa ctt ggc aac gaa tct gac aag tta caa gta gtc ttt ata act	336

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Asp Gln Leu Gly Asn Glu Ser Asp Lys Leu Gln Val Val Phe Ile Thr
    100                      105                      110

att gat cca aca aaa gat act gta gaa aca cta aaa gag ttt cac aaa   384
Ile Asp Pro Thr Lys Asp Thr Val Glu Thr Leu Lys Glu Phe His Lys
    115                      120                      125

aat ttt gac tca cgg att caa atg tta aca gga aac att gaa gct att   432
Asn Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Ile Glu Ala Ile
    130                      135                      140

aat caa ata gta caa ggg tac aaa gta tat gta ggt cag cca gac aat   480
Asn Gln Ile Val Gln Gly Tyr Lys Val Tyr Val Gly Gln Pro Asp Asn
    145                      150                      155                      160

gat aac caa att aac cat tct gga ata atg tat att gta gac aag aaa   528
Asp Asn Gln Ile Asn His Ser Gly Ile Met Tyr Ile Val Asp Lys Lys
    165                      170                      175

gga gaa tat tta aca cat ttt gta cca gat tta aag tca aaa gag cct   576
Gly Glu Tyr Leu Thr His Phe Val Pro Asp Leu Lys Ser Lys Glu Pro
    180                      185                      190

caa gtg gat aaa tta ctt tct tta att aag cag tat ctt taa           618
Gln Val Asp Lys Leu Leu Ser Leu Ile Lys Gln Tyr Leu
    195                      200                      205

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&lt;210&gt; 26

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Cowdria ruminantium

&lt;400&gt; 26

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Met Lys Ala Ile Lys Phe Ile Leu Asn Leu Cys Leu Leu Phe Ala Ala
  1                      5                      10                      15

Ile Phe Leu Gly Tyr Ser Tyr Ile Thr Lys Gln Gly Ile Phe Gln Pro
    20                      25                      30

Lys Leu His Asp Ser Pro Asp Val Asn Ile Ser Asn Lys Ala Asp Ile
    35                      40                      45

Asn Thr Ser Phe Ser Leu Ile Asn Gln Asp Gly Ile Thr Ile Ser Ser
    50                      55                      60

Lys Asp Phe Leu Gly Lys His Met Leu Val Leu Phe Gly Phe Ser Ser
    65                      70                      75                      80

Cys Lys Thr Ile Cys Pro Met Glu Leu Gly Leu Ala Ser Thr Ile Leu
    85                      90                      95

Asp Gln Leu Gly Asn Glu Ser Asp Lys Leu Gln Val Val Phe Ile Thr
    100                      105                      110

Ile Asp Pro Thr Lys Asp Thr Val Glu Thr Leu Lys Glu Phe His Lys

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115	120	125
Asn Phe Asp Ser Arg Ile Gln Met Leu Thr Gly Asn Ile Glu Ala Ile		
130	135	140
Asn Gln Ile Val Gln Gly Tyr Lys Val Tyr Val Gly Gln Pro Asp Asn		
145	150	155
Asp Asn Gln Ile Asn His Ser Gly Ile Met Tyr Ile Val Asp Lys Lys		
	165	170
Gly Glu Tyr Leu Thr His Phe Val Pro Asp Leu Lys Ser Lys Glu Pro		
	180	185
Gln Val Asp Lys Leu Leu Ser Leu Ile Lys Gln Tyr Leu		
195	200	205

&lt;210&gt; 27

&lt;211&gt; 981

&lt;212&gt; DNA

&lt;213&gt; Cowdria ruminantium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (978)

&lt;400&gt; 27

atg aag aaa ata ttg gtt acg ttt tta gtt gtt gtt aat gtg ttt tgt	48
Met Lys Lys Ile Leu Val Thr Phe Leu Val Val Val Asn Val Phe Cys	
1 5 10 15	
aat gct gcc att gct tca act gac tca tca gaa gat aaa cag tat att	96
Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile	
20 25 30	
tta att ggt act ggt tct atg act gga gta tat tat cct ata gga ggt	144
Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly	
35 40 45	
agc ata tgt agg ttt att gca tct gat tat ggt aat gat aat aac agc	192
Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser	
50 55 60	
ata gtt tgt tct ata tct tct aca act ggt agc gta tat aat ctt aat	240
Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn	
65 70 75 80	
tct atg cgt tat gca aat atg gat ata ggt att att caa tct gat tta	288
Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu	
85 90 95	
gag tac tat gca tat aat ggt att ggt tta tat gaa aaa atg cca gca	336
Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala	
100 105 110	



atg agg cat cta aga ata tta tct tca tta cat aaa gaa tat ctt aca	384
Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr	
115 120 125	
att gtt gtt agg gcg aat tct aat ata tca gtt att gat gat ata aaa	432
Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys	
130 135 140	
ggc aaa aga gtt aat att ggt agt cct ggt act ggt gta aga ata gca	480
Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala	
145 150 155 160	
atg tta aaa ttg tta aat gaa aaa gga tgg gga aga aaa gat ttt gct	528
Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala	
165 170 175	
gtt atg gca gaa tta aaa tca tca gag caa gct caa gca tta tgt gat	576
Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp	
180 185 190	
aat aaa att gat gtg atg gta gat gtt gtt gga cat cct aat gct gca	624
Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala	
195 200 205	
att caa gaa gca gca gca act tgt gat ata aaa ttt att tct tta gat	672
Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp	
210 215 220	
gat gat ctc ata gat aaa tta cat act aag tat ccc tat tat aaa agg	720
Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg	
225 230 235 240	
gat att att agt ggt gcg tta tac agt aac tta cct gat ata caa act	768
Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr	
245 250 255	
gtt tca gta aaa gct tct tta ata aca act act gaa tta agc aat gag	816
Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu	
260 265 270	
ttg gcc tat aaa gtt gtt aaa tct ttg gtt agc cat tta cat gaa cta	864
Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu	
275 280 285	
cat gga att act gga gct ctt aga aat ctt act gta aaa gac atg gta	912
His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val	
290 295 300	
cag tca gat att aca cct tta cat gac ggt gca aaa cgt tat tat aag	960
Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys	
305 310 315 320	
gaa att gga gtt ata aaa taa	981
Glu Ile Gly Val Ile Lys	
325	

<210> 28  
 <211> 326  
 <212> PRT  
 <213> Cowdria ruminantium

<400> 28  
 Met Lys Lys Ile Leu Val Thr Phe Leu Val Val Val Asn Val Phe Cys  
   1                  5                  10                  15  
 Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile  
                   20                  25                  30  
 Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly  
           35                  40                  45  
 Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser  
   50                  55                  60  
 Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn  
   65                  70                  75                  80  
 Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu  
                   85                  90                  95  
 Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala  
           100                  105                  110  
 Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr  
   115                  120                  125  
 Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys  
   130                  135                  140  
 Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala  
   145                  150                  155                  160  
 Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala  
                   165                  170                  175  
 Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp  
           180                  185                  190  
 Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala  
   195                  200                  205  
 Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp  
   210                  215                  220  
 Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg  
   225                  230                  235                  240  
 Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr  
           245                  250                  255  
 Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu

260	265	270
Leu Ala Tyr Lys Val Val Lys Ser	Leu Val Ser His	Leu His Glu Leu
275	280	285
His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val		
290	295	300
Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys		
305	310	315
Glu Ile Gly Val Ile Lys		
325		

<210> 29  
 <211> 519  
 <212> DNA  
 <213> Cowdria ruminantium

<220>  
 <221> CDS  
 <222> (1)..(516)

<400> 29	
atg aat ata ttc aat tat atg cag ata atg cct aat ata agt gtt gat	48
Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp	
1 5 10 15	
gca ttt gtt gca cct act gct gta att ata ggt gat gtt tgt gta aat	96
Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn	
20 25 30	
gac aag tgt agc att tgg tat aac tca gta tta cgt gga gat gta ggc	144
Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly	
35 40 45	
caa att gtt att ggt gta ggt act aat att caa gat ggg aca ata ata	192
Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile	
50 55 60	
cat gtt gat agg aaa tat ggt aat acg aat att ggc aaa aag gtt act	240
His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr	
65 70 75 80	
att ggg cat ggg tgt ata tta cat gct tgt gag ata caa gat tat gtg	288
Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val	
85 90 95	
ctt gtt gga atg gga tct att att atg gat aac gtt gtg gtt gaa aag	336
Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys	
100 105 110	
aat gca atg gtg gct gct gga tca tta gtg gta aga ggt aaa gtt gtg	384
Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val	
115 120 125	

aaa act ggt gaa tta tgg gct ggt agg cct gca caa ttt tta aga atg 432  
 Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met  
           130                          135                          140

ttg tct agt gat gaa att aaa gag ata agt aaa tct gct gat aac tat 480  
 Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr  
           145                          150                          155                          160

ata gag ctt gcc agt gat tac ata act ggt aag ttg taa 519  
 Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu  
                                   165                                  170

<210> 30

<211> 172

<212> PRT

<213> Cowdria ruminantium

<400> 30

Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp  
           1                          5                          10                          15

Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn  
                           20                          25                          30

Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly  
                           35                          40                          45

Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile  
           50                          55                          60

His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr  
           65                          70                          75                          80

Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val  
                           85                          90                          95

Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys  
                           100                          105                          110

Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val  
           115                          120                          125

Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met  
           130                          135                          140

Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr  
           145                          150                          155                          160

Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu  
                           165                          170

<210> 31

<211> 753

&lt;212&gt; DNA

&lt;213&gt; Cowdria ruminantium

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(750)

&lt;400&gt; 31

atg atg ata aga atc ttt ctt ttg tta ggc tta gta tta tta gta gca	48
Met Met Ile Arg Ile Phe Leu Leu Leu Gly Leu Val Leu Leu Val Ala	
1 5 10 15	
agt ttt cca cta tta aat aac tgg cta tct aat cat tct ggt aag tct	96
Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser	
20 25 30	
act aca ttg gat aag gat gca gtt ata tct ata gtt gag gaa tat ata	144
Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile	
35 40 45	
acc aat tat cct cag agg gta ata gat tta ctt act aca ggc caa gca	192
Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala	
50 55 60	
caa gca gaa aga gca gag ctt act gaa aat att aaa aaa tat aaa tct	240
Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser	
65 70 75 80	
gag ctt gaa gat att gca tac cca tct gct ggc aat aaa gac agt aaa	288
Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys	
85 90 95	
att gca ttt att gag ttc ttc gat tac tct tgt ggt tat tgt aaa atg	336
Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met	
100 105 110	
atg ttt gaa gat atc aaa caa att ata aaa gat ggt aag gta cgt gtt	384
Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val	
115 120 125	
att ttt aga gat ttt cca ata ctt ggg gaa tcg tcg tta aag gct gtt	432
Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val	
130 135 140	
aaa gca gca ttg gct gta cat ctt atc aat cca agt aaa tac ttg gac	480
Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp	
145 150 155 160	
ttc tat tat gca gca tta aat cat aaa cag cca ttt aat gat gaa tct	528
Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser	
165 170 175	
ata ctt aat ata gtt aaa tca ctt gaa att tca gaa gag gaa ttt aaa	576
Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys	
180 185 190	

gat tct tta tct aaa aat tct agt act att gat aag atg ata gag tcc 624  
Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser  
195 200 205  
  
act aga aat ctg gct gag aag tta aat atc aga ggt act cct gct ctt 672  
Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu  
210 215 220  
  
ata ata ggt gat gca ttc att ggg gga gct gca gat tta tca act tta 720  
Ile Ile Gly Asp Ala Phe Ile Gly Gly Ala Ala Asp Leu Ser Thr Leu  
225 230 235 240  
  
aga agt aaa ata gta gaa cag cag gaa caa taa 753  
Arg Ser Lys Ile Val Glu Gln Gln Glu Gln  
245 250

<210> 32  
<211> 250  
<212> PRT  
<213> Cowdria ruminantium

<400> 32  
Met Met Ile Arg Ile Phe Leu Leu Leu Gly Leu Val Leu Leu Val Ala  
1 5 10 15  
  
Ser Phe Pro Leu Leu Asn Asn Trp Leu Ser Asn His Ser Gly Lys Ser  
20 25 30  
  
Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile  
35 40 45  
  
Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala  
50 55 60  
  
Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser  
65 70 75 80  
  
Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys  
85 90 95  
  
Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met  
100 105 110  
  
Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val  
115 120 125  
  
Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val  
130 135 140  
  
Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp  
145 150 155 160  
  
Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser  
165 170 175

Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys  
 180 185 190

Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser  
 195 200 205

Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu  
 210 215 220

Ile Ile Gly Asp Ala Phe Ile Gly Gly Ala Ala Asp Leu Ser Thr Leu  
 225 230 235 240

Arg Ser Lys Ile Val Glu Gln Gln Glu Gln  
 245 250

<210> 33  
 <211> 450  
 <212> DNA  
 <213> Cowdria ruminantium

<220>  
 <221> CDS  
 <222> (1) .. (447)

<400> 33  
 atg cat aga tca aat att att gaa att ttt ata gga ttc cta gtg tta 48  
 Met His Arg Ser Asn Ile Ile Glu Ile Phe Ile Gly Phe Leu Val Leu  
 1 5 10 15

gca gga gca ata tct att ggg ata ata gca ttt aac aaa tta cca tat 96  
 Ala Gly Ala Ile Ser Ile Gly Ile Ile Ala Phe Asn Lys Leu Pro Tyr  
 20 25 30

aaa aat acc ttg cgt aat tgt tat aca gtt aaa gca ttt ttc tca aat 144  
 Lys Asn Thr Leu Arg Asn Cys Tyr Thr Val Lys Ala Phe Phe Ser Asn  
 35 40 45

gta gat ggg ttg gac ata gga gat gaa gta aca ata tca gga gta aaa 192  
 Val Asp Gly Leu Asp Ile Gly Asp Glu Val Thr Ile Ser Gly Val Lys  
 50 55 60

ata ggt aca gta act tca ata tca ttg aat gaa agc tat act cct ata 240  
 Ile Gly Thr Val Thr Ser Ile Ser Leu Asn Glu Ser Tyr Thr Pro Ile  
 65 70 75 80

gta aca atg tgc ata cag aaa aat atc tta cta cct tca gat agt tca 288  
 Val Thr Met Cys Ile Gln Lys Asn Ile Leu Leu Pro Ser Asp Ser Ser  
 85 90 95

gca tct ata tta aac agc aat atg tta gga aaa aag cac att gat atc 336  
 Ala Ser Ile Leu Asn Ser Asn Met Leu Gly Lys Lys His Ile Asp Ile  
 100 105 110

gaa ctt gga tca gat caa gaa gtc atc gta agt gaa ggt tta ata gaa 384  
 Glu Leu Gly Ser Asp Gln Glu Val Ile Val Ser Glu Gly Leu Ile Glu

115                      120                      125  
 cat aca cat tca gat tta agt ttc aat gca att att gct aaa ata ata 432  
 His Thr His Ser Asp Leu Ser Phe Asn Ala Ile Ile Ala Lys Ile Ile  
     130                      135                      140  
  
 gat tca ctt att aag tag 450  
 Asp Ser Leu Ile Lys  
 145

<210> 34  
 <211> 149  
 <212> PRT  
 <213> Cowdria ruminantium

<400> 34  
 Met His Arg Ser Asn Ile Ile Glu Ile Phe Ile Gly Phe Leu Val Leu  
     1                      5                      10                      15  
  
 Ala Gly Ala Ile Ser Ile Gly Ile Ile Ala Phe Asn Lys Leu Pro Tyr  
             20                      25                      30  
  
 Lys Asn Thr Leu Arg Asn Cys Tyr Thr Val Lys Ala Phe Phe Ser Asn  
             35                      40                      45  
  
 Val Asp Gly Leu Asp Ile Gly Asp Glu Val Thr Ile Ser Gly Val Lys  
     50                      55                      60  
  
 Ile Gly Thr Val Thr Ser Ile Ser Leu Asn Glu Ser Tyr Thr Pro Ile  
     65                      70                      75                      80  
  
 Val Thr Met Cys Ile Gln Lys Asn Ile Leu Leu Pro Ser Asp Ser Ser  
             85                      90                      95  
  
 Ala Ser Ile Leu Asn Ser Asn Met Leu Gly Lys Lys His Ile Asp Ile  
             100                      105                      110  
  
 Glu Leu Gly Ser Asp Gln Glu Val Ile Val Ser Glu Gly Leu Ile Glu  
     115                      120                      125  
  
 His Thr His Ser Asp Leu Ser Phe Asn Ala Ile Ile Ala Lys Ile Ile  
     130                      135                      140  
  
 Asp Ser Leu Ile Lys  
 145